

1 TCAAATTTTT CTCCAGTTCT AAATATCCGG AACCTCTTG GGATGCCATT  
51 GCCCATCTAT CTGTAATTTA TTGACGAAAT AGACGAAAAG GAAGGTGGCT  
101 CCTATAAAGC ACATCATTGC GATAACAGAA AGGCCATTGT TGAAGATACC  
151 TCTGCTGACA TTGGTCCCCA AGTGGAAGCA CCACCCCATG AGGAGCACCG  
201 TGGAGTAAGA AGACGTTCGA GCCACGTCGA AAAAGCAAGT GTGTTGATGT  
251 AGTATCTCCA TTGACGTAAG GGATGACGCA CAATCCAAC TATCCATCGCA  
301 AGACCATTGC TCTATATAAG AAAGTTAATA TCATTTCGAG TGGCCACGCT  
351 G [SEQ ID NO:2]

FIGURE 2